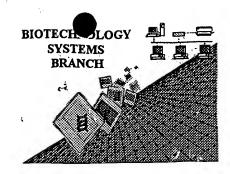
RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

| Application Serial Number: | 09/84/, 321 |
|----------------------------|-------------|
| Source: | OIPE |
| Date Processed by STIC: | 5/11/2001 |

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-368-4216. PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax) PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER</u> <u>VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

http://www.uspto.gov/web/offices/pac/checker

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/84/, 321

| ATTN: | | LEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE |
|-----------------|------------------------------------|--|
| 1 | Wrapped Nucleics | The number/text at the end of each line "wrapped" down to the next line. |
| | | This may occur if your file was retrieved in a word processor after creating it. |
| | | Please adjust your right margin to .3, as this will prevent "wrapping". |
| 2 | Wrapped Aminos | The amino acid number/text at the end of each line "wrapped " down to the next line. |
| | | This may occur if your file was retrieved in a word processor after creating it. |
| | | Please adjust your right margin to .3, as this will prevent "wrapping". |
| 3 | Incorrect Line Length | The rules require that a line not exceed 72 characters in length. This includes spaces. |
| 4 | Micelianed Amine Asid | The numbering under each 5th amine said is misslighted. This may be caused by the use of table |
| 4 | Misaligned Amino Acid Numbering | The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers. |
| _ | N | This firms and any distance of the Application of t |
| 5 | Non-ASCIi | This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. |
| | | Please ensure your subsequent submission is saved in ASCII text so that it can be processed. |
| 6 | Variable Length | Sequence(s) contain n's or Xaa's which represented more than one residue. |
| | | As per the rules, each n or Xan can only represent a single residue. |
| | | Please present the maximum number of each residue having variable length and |
| | | indicate in the (ix) feature section that some may be missing. |
| 7 | Patentin ver. 2.0 "bug" | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid |
| | | sequence(s) Normally, Patentin would automatically generate this section from the |
| | | previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section |
| | | to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> |
| | | sections for Artificial or Unknown sequences. |
| • | 011 | |
| 8 | Skipped Sequences | Sequence(s) missing. If intentional, please use the following format for each skipped sequence: |
| | (OLD RULES) | (2) INFORMATION FOR SEQ ID NO:X: (3) SEQUENCE CHARACTERISTICS:(Do not insert any boodings under "SEQUENCE CHARACTERISTICS") |
| | | (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS") (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: |
| | | This sequence is intentionally skipped |
| | | This sequence is intentionally shipped |
| | ; | Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s). |
| 9 | Skipped Sequences | Sequence(s) missing. If intentional, please use the following format for each skipped sequence. |
| | (NEW RULES) | <210> sequence id number |
| | (, | <400> sequence id number |
| | | 000 |
| • | | |
| 10 | Use of n's or Xaa's | Use of n's and/or Xaa's have been detected in the Sequence Listing. |
| | (NEW RULES) | Use of <220> to <223> is MANDATORY if n's or Xaa's are present. |
| | | In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents. |
| 11 | Use of "Artificia!" | Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. |
| \mathcal{T} | (NEW RULES) | Valid response is Artificial Sequence. |
| . / | | 1-18 (and more) |
| 12 0 | Use of <220>Feature | Sequence(s) are missing the <220>Feature and associated headings. |
| | (NEW RULES) | Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown" |
| | | Please explain source of genetic material in <220> to <223> section. |
| | | (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules) |
| 13 [·] | Patentin ver. 2.0 "bug" | Please do not use "Copy to Disk" function f Patentln versi n 2.0. This causes a corrupted |
| | | file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). |
| | | Instead, please use "File Manager" or any other means to copy file to floppy disk. |
| | • | military, process and manager of any time means to dopy me to hoppy distin |

AMC - Biotechnology Systems Branch - 4/06/2001

OIPE

```
pr 1-5
                     Output Set: N:\CRF3\05112001\I841321.raw
      3 <110> APPLICANT: Urry, Dan
      5 <120> TITLE OF INVENTION: Injectable Implants For Tissue Augmentation and Restoration
      7 <130> FILE REFERENCE: BERL-020/04US
      9 <140> CURRENT APPLICATION NUMBER: US/09/841,321
      9 <141> CURRENT FILING DATE: 2001-04-23
      9 <150> PRIOR APPLICATION NUMBER: US 09/258,723
     10 <151> PRIOR FILING DATE: 1999-02-26
                                                                          Does Not Comply
     12 <150> PRIOR APPLICATION NUMBER: US 60/087155
                                                                     Corrected Diskette Needed
     13 <151> PRIOR FILING DATE: 1998-05-29
     15 <150> PRIOR APPLICATION NUMBER: US 60/076297
     16 <151> PRIOR FILING DATE: 1998-02-27
     18 <160> NUMBER OF SEQ ID NOS: 65
     20 <170> SOFTWARE: PatentIn version 3.0
                                                sel tem 12 on Evan Surmay Sheet
(global evan)
     22 <210> SEQ ID NO: 1
     23 <211> LENGTH: 180
     24 <212> TYPE: DNA
25 <213 ORGANISM:
W--> 27 (220) FEATURE:
                       Artificial Sequence
W--> 27 (<223>) OTHER INFORMATION:
     27 400 SEQUENCE: 1
     28 gaggarcega agacaacagg tygtgtteeg ggeggegtae egggtggegt acegggeggt
     30 ttecegggag gtgtqeeggg tggggtteea ggeggtgtae egggtgqgtt teegggeggt
                                                                              120
     32 gttccgggtg gagttccggg tggcgtgccg ggcggttttc caggaagtct tcggatccag
                                                                              180
     35 <210> SEQ ID NO: 2
     36 <211> LENGTH: 113
     37 <212> TYPE: DNA
     38 <213 ORGANISM: (Artificial Sequence
W--> 40/<220> FEATURE:
W--> 40 <223 > OTHER INFORMATION:
        40
     41 gaggatecaq gegttggggt accgggtgtt ggegtacegg gtaaaggtgt ecegggegtt
                                                                               60
     43 gytgtgccgg gigtaggctt tccgggtttc ggattcccag gcgttggatc cag
                                                                              113
     46 <210> SEQ ID NO: 3
     47 <211> LENGTH: 33
     48 <212> TYPE: DNA-
     49 <213 ORGANISM: Artificial Sequence
W--> 51 <220> FEATURE:
W--> 51(<223>OTHER INFORMATION:
     51 <400> SEQUENCE: 3
     52 taggggtacc gggtcgtggt gactctccgg gcg
                                                                               33
     55 <210> SEQ ID NO: 4
     56 <211> LENGTH: 33
     57 <212> TYPE: DNA
     59 213 ORGANISM (Artificial Sequence
W--> 60(<220>) FEATURE:
w--> 60/
       <223 OTHER INFORMATION:
     60 <400> SEQUENCE: 4
```

DATE: 05/11/2001

TIME: 11:46:49

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/841,321

Input Set : A:\BERL 020.04.txt

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/841,321

Input Set : A:\BERL 020.04.txt
Output Set: N:\CRF3\05112001\I841321.raw

DATE: 05/11/2001

TIME: 11:46:49

```
61 cgcatcccca tggcccagca ccactgagag gcc
                                                                               33
     64 <210> SEQ ID NO: 5
     65 <211> LENGTH: 111
     66 <212> TYPE: DNA
     67 <213 ORGANISM (Artificial Sequence
W--> 69/<220> FEATURE:
W--> 69 <223 OTHER INFORMATION:
     69 <400> SEQUENCE: 5
     70 gaggatccag gcgttggggt accgggtgtt ggcgtaccgg gtgttggtgt cccgggcaaa
                                                                               60
     72 ggtgtgccgg gtgtaggcgt tccgggtgtg ggagtcccag gcgttggatc c
                                                                              111
     75 <210> SEQ ID NO: 6
     76 <211> LENGTH: 345
     77 <212 TYPE: DNA
  78 <213> ORGANISM: Artificial Sequence
  -> 80 <223> OTHER INFORMATION:
     88 <400 SEQUENCE: 6
     81 ggcgttggtg taccgggtgt tggtgtgccg ggtgttggtg ttccgggcgt aggcgtaccg
                                                                               60
     83 ggcgtaggeg tgccgggcgt aggcgttccg ggcgtgggcg taccgggcgt gggcgtgccg
                                                                              120 .
     85 ggtgtgggeg tecegggtgt aggtgtteea ggegtagggg tacegggteg tggtgaetet
                                                                              180
     87 cogggogttg gtgtacoggg tgttggtgtg cogggtgttg gtgttccggg cgtaggcgta
                                                                              240
                                                                              300
     89 ccgggcgtag gcgtgccggg cgtaggcgtt ccgggcgtgg gcgtaccggg cgtgggcgtg
     91 ccgggtgtgg gcgtcccggg tgtaggtgtt ccaggcgttg gatcc
                                                                              345
     94 <210> SEQ ID NO: 7
     95 <211> LENGTH: 463
     96 <212> TYPE: DNA
     97 13 ORGANISM: Artificial Sequence
W--> 99/<220>)FEATURE:
W--> 99 <223 ✓ OTHER INFORMATION:
     99 <400> SEQUENCE: 7
     100 ggatecagge gttggtgtae egggtgttgg tgtgeegggt gttggtgtte egggegtagg
                                                                                60
     102 cgtaccgggc gtaggcgtgc cgggcgtagg cgttccgggc gtgggcgtac cgggcgtggg
                                                                               120
     104 cgtgccgggt gtgggcgtcc caggtgtagg cgttccgggt gtgggtgtag ctccgggtgt
                                                                               180
     106 tggcgttgca ccgggcgtag gtgttgctcc gggcgttggc gtggcgccgg gtgttggtgt
                                                                               240
     108 tgctccgggt gtaggcgttg ctccgggcgt tggtgttgcc ccaggtgtag gtgtggcacc
                                                                               300
     110 gggcgttggt gtaccgggtg ttggtgtgcc gggtgttggt gttccgggcg taggcgtacc
                                                                               360
     112 gggcgtaggc gtgccgggcg taggcgttcc gggcgtggcc gtaccgggcg tgggcgtgcc
                                                                               420
     114 gggtgtgggc gtcccgggtg taggtgttcc aggcgttgga tcc
                                                                               463
     117 <210> SEQ ID NO: 8
     118 <211> LENGTH: 111
     119 <212> TYPE: DNA
     120 <213 ORGANISM Artificial Sequence
W--> 122/ <220 FEATURE:
W--> 122 <223 OTHER INFORMATION:
     122 <400> SEQUENCE: 8
     123 gaggatccag gcgttggggt accgggtgtt ggcgtaccgg gtgaaggtgt cccgggcgtt
                                                                                60
     125 ggtgtgccgg gtgtaggcgt tccgggtgtg ggagtcccag gcgttggatc c
                                                                               111
     128 <210> SEQ ID NO: 9
     129 <211> LENGTH: 48
```

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TIME: 11:46:49

```
Input Set : A:\BERL 020.04.txt
                      Output Set: N:\CRF3\05112001\1841321.raw
      130 <212> TYPE: PRT
     131 /213> ORGANISM: Artificial Sequence
W--> 133 <220 FEATURE:
   -> 133 <223 OTHER INFORMATION:
      133 <400> SEQUENCE: 9
      135 Gly Gly Val Pro Gly Gly Val Pro Gly Gly Val Pro Gly Gly Phe Pro
     138 Gly Gly Val Pro Gly Gly Val Pro Gly Gly Val Pro Gly Gly Phe Pro
                      20
                                            25
     139
     141 Gly Gly Val Pro Gly Gly Val Pro Gly Val Pro Gly Gly Phe Pro
                  35
     144 <210> SEQ ID NO: 10
     145 <211> LENGTH: 30
     146 <212> TYPE: PRT
     147 SAR ORGANISM: Artificial Sequence
W--> 149 <220> FEATURE:
W--> 149 <223≯ OTHER INFORMATION:
     149 <400> SEQUENCE: 10
     151 Gly Val Gly Val Pro Gly Val Gly Vaí Pro Gly Lys Gly Val Pro Gly
     152 1
                          5
                                                10
     154 Val Gly Val Pro Gly Val Gly Phe Pro Gly Phe Gly Phe Pro
                      20
     155
     157 <210> SEQ ID NO: 11
     158 <211> LENGTH: 11
     159 <212> TYPE: PRT
     160 MGANISM Artificial Sequence
W--> 162/<220> FEATURE:
W--> 162 <223 > OTHER INFORMATION:
     162 <400> SEQUENCE: 11
     164 Val Gly Val Pro Gly Arg Gly Asp Ser Pro Gly
     135 1
     167 <210> SEQ ID NO: 12
     168 <211> LENGTH: 30
     169 <212> TYPE: PRT/
170 <213 ORGANISM: Artificial Sequence W--> 172 <220 FEATURE: W--> 172 <223 OTHER INFORMATION:
     172 <400> SEQUENCE: 12
     174 Gly Val Gly Val Pro Gly Val Gly Val Pro Gly Lys Gly Val Pro Gly
     177 Val Gly Val Pro Gly Val Gly Val Pro Gly Val Gly Val Pro
     178
                      20
     180 <210> SEQ ID NO: 13
     181 <211> LENGTH: 111
     182 <212> TYPE: PRT
     183 213 ORGANISM Artificial Sequence
W--> 185 (220) FEATURE:
W--> 185 (223) OTHER INFORMATION:
     165 <400> SEQUENCE: 13
```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/841,321

DATE: 05/11/2001

TIME: 11:46:49

```
PATENT APPLICATION: US/09/841,321
                     Input Set : A:\BERL 020.04.txt
                     Output Set: N:\CRF3\05112001\1841321.raw
     187 Gly Val Gly Val Pro Gly Val Gly Val Pro Gly Val Gly Val Pro Gly
     190 Val Gly Val Pro Gly Val Gly Val Pro Gly Val Gly Val Pro Gly Val
                     20
                                         25
     193 Gly Val Pro Gly Val Gly Val Pro Gly Val Gly Val Pro Gly Val Gly
                35
                                     40
     196 Val Pro Gly Val Gly Val Pro Gly Arg Gly Asp Ser Pro Gly Val Gly
     197
             50
                                 55
     199 Val Pro Gly Val Gly Val Pro Gly Val Pro Gly Val Gly Val
                                                 75
     202 Pro Gly Val Gly Val Pro Gly Val Gly Val Pro Gly Val Gly Val Pro
                                             90
     205 Gly Val Gly Val Pro Gly Val Gly Val Pro Gly Val Gly Val Pro
     206
                     100
                                        105
     208 <210> SEQ ID NO: 14
     209 <211> LENGTH: 148
     210 <212> TYPE: PRT
     211 <216 ORGANISM (Artificial Sequence)
W--> 213 <220> FEATURE:
W--> 213 <223> OTHER INFORMATION:
     213 400 SEQUENCE: 14
     215 Gly Val Gly Val Pro Gly Val Gly Val Pro Gly Val Fro Gly
     218 Val Gly Val Pro Gly Val Gly Val Pro Gly Val Gly Val Pro Gly Val
                    20
     221 Gly Val Pro Gly Val Gly Val Pro Gly Val Gly Val Pro Gly Val Gly
     224 Val Pro Gly Val Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly Val
     227 Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly Val Ala Pro
                            70
                                                75
     230 Gly Val Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly Val
                         85
     233 Ala Pro Gly Val Gly Val Pro Gly Val Pro Gly Val Gly Val
                                        105
     236 Pro Gly Val Gly Val Pro Gly Val Gly Val Pro Gly Val Gly Val Pro
     237
                115
                                    120
     239 Gly Val Gly Val Pro Gly Val Gly Val Pro Gly Val Gly Val Pro Gly
            130
                                135
     242 Val Gly Val Pro
     243 145
     245 <210> SEQ ID NO: 15
     246 <211> LENGTH: 30
     247 <212> TYPE: PRT
     248 <213> QRGANISM:(Artificial Sequence)
W--> 250 <220> PEATURE:
W--> 250 223 OTHER INFORMATION:
     250 <400> SEQUENCE: 15
     252 Gly Val Gly Val Pro Gly Val Gly Val Pro Gly Glu Gly Val Pro Gly
```

RAW SEQUENCE LISTING

DATE: 05/11/2001

```
PATENT APPLICATION: US/09/841,321
                                                                TIME: 11:46:49
                      Input Set : A:\BERL 020.04.txt
                      Output Set: N:\CRF3\05112001\1841321.raw
     253 1
     255 Val Gly Val Pro Gly Val Gly Val Pro Gly Val Gly Val Pro
     256
                      20
     258 <210> SEQ ID NO: 16
     259 <211> LENGTH: 4
     260 <212> TYPE: PRT
261 <213 ORGANISM Artificial Sequence W--> 263 (220) FEATURE:
W--> 263 <223 > OTHER INFORMATION:
     263 <400> SEQUENCE: 16
     265 Val Pro Gly Gly
     266 1
     268 <210> SEQ ID NO: 17
     269 <211> LENGTH: 5
     270 <212> TYPE: PRT
271 <213 ORGANISM: Artificial Sequence W--> 273 <220) FEATURE:
W--> 278 <223 OTHER INFORMATION:
     273 <400> SEQUENCE: 17
     275 Val Pro Gly Val Gly
     276 1
     278 <210> SEQ ID NO: 18
     279 <211> LENGTH: 1255
     280 <212> TYPE: PRT_
     281 273> ORGANISM Artificial Sequence
W--> 283/ <220> FEATURE:
W--> 283 <223> OTHER INFORMATION: 283 <400> SEQUENCE: 18
     285 Gly Val Gly Val Pro Cly Val Gly Val Pro Gly Val Cly Val Pro Gly
     288 Val Gly Val Pro Cly Val Gly Val Pro Gly Val Gly Val Pro Gly Val
     291 Gly Val Pro Gly Val Gly Val Pro Gly Val Gly Val Pro Gly Val Gly
     294 Val Pro Gly Val Gly Val Pro Gly Val Gly Val Pro Gly Val Gly Val
     297 Pro Gly Val Gly Val Pro Gly Val Gly Val Pro Gly Val Gly Val Pro
     298 65
     300 Gly Val Gly Val Pro Gly Val Gly Val Pro Gly Val Gly Val Pro Gly
                                               90
     303 Val Gly Val Pro Gly Val Gly Val Pro Gly Val Gly Val Pro Gly Val
                                           105
     306 Gly Val Pro Gly Val Gly Val Pro Gly Val Gly Val Pro Gly Val Gly
                 115
     309 Val Pro Gly Val Gly Val Pro Gly Val Gly Val Pro Gly Val Gly Val
                                  135
     312 Pro Gly Val Gly Val Pro Gly Val Gly Val Pro Gly Val Gly Val Pro
                              150
                                                   155
     315 Gly Val Gly Val Pro Gly Val Gly Val Pro Gly Val Gly Val Pro Gly
```

RAW SEQUENCE LISTING

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

VERIFICATION SUMMARY

DATE: 05/11/2001 TIME: 11:46:50

PATENT APPLICATION: US/09/841,321

Input Set : A:\BERL 020.04.txt

Output Set: N:\CRF3\05112001\1841321.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date L:27 M:258 W: Mandatory Feature missing, <220> FEATURE: L:27 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: L:40 M:258 W: Mandatory Feature missing, <220> FEATURE: L:40 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: L:51 M:258 W: Mandatory Feature missing, <220> FEATURE: L:51 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: L:60~M:258~W: Mandatory Feature missing, <220> FEATURE: $L:60\ M:258\ W:$ Mandatory Feature missing, <223> OTHER INFORMATION: L:69 M:258 W: Mandatory Feature missing, <220> FEATURE: L:69 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: L:80 M:258 W: Mandatory Feature missing, <220> FEATURE: L:80 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: L:99 M:258 W: Mandatory Feature missing, <220> FEATURE: L:99 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: L:122 M:258 W: Mandatory Feature missing, <220> FEATURE: L:122 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: L:133 M:258 W: Mandatory Feature missing, <220> FEATURE: L:133 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: $L:149\ M:258\ W:$ Mandatory Feature missing, <220> FEATURE: L:149 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: L:162 M:258 W: Mandatory Feature missing, <220> FEATURE: L:162 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: L:172 M:258 W: Mandatory Feature missing, <220> FEATURE: L:172 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: L:185 M:258 W: Mandatory Feature missing, <220> FEATURE: L:185 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: L:213 M:258 W: Mandatory Feature missing, <220> FEATURE: L:213 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: L:250 M:258 W: Mandatory Feature missing, <220> FEATURE: L:250 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: L:263 M:258 W: Mandatory Feature missing, <220> FEATURE: $\label{eq:L:263} L{:}\,263~M{:}\,258~W{:}~\texttt{Mandatory}~\texttt{Feature}~\texttt{missing},~\texttt{<223>}~\texttt{OTHER}~\texttt{INFORMATION}{:}$ L:273 M:258 W: Mandatory Feature missing, <220> FEATURE: L:273 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: L:283 M:258 W: Mandatory Feature missing, <220> FEATURE: L:283 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: L:539 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 L:547 M:258 W: Mandatory Feature missing, <220> FEATURE: L:547 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: L:557 M:258 W: Mandatory Feature missing, <220> FEATURE: L:557 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: L:597 M:258 W: Mandatory Feature missing, <220> FEATURE: L:597 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: $L:610\ M:258\ W:$ Mandatory Feature missing, <220> FEATURE: L:610 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: L:638 M:258 W: Mandatory Feature missing, <220> FEATURE:

Input Set : A:\BERL 020.04.txt
Output Set: N:\CRF3\05112001\I841321.raw

L:638 M:258 W: Mandatory, Feature missing, <223> OTHER INFORMATION: L:649 M:258 W: Mandatory Feature missing, <220> FEATURE: L:649 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: L:776 M:258 W: Mandatory Feature missing, <220> FEATURE: L:776 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: